

 MASCOT Search Results

User : Ulf Bergmann
E-mail : ub@pfa
Search title : 24B026, Univ Kiel, Hering-Peter, Sample 1 (10 ppm)
MS data file : LTQ_24B026_UnivKiel_Sample1_10ul.mgf
Databases : **1:** contaminants 20160129 (250 sequences; 129,192 residues)
2: SwissProt 2024_02 (571,282 sequences; 206,678,396 residues)
3: UB_target (60,791 sequences; 29,305,254 residues)
Timestamp : 30 Apr 2024 at 11:33:46 GMT

[All](#) [Non-significant](#) [Unassigned](#) [🔗\[help\]](#) [As](#) [XML](#)

Not what you expected? Try [🔗the select summary](#).

- ▶ **Search parameters**
- ▶ **Score distribution**
- ▶ **Modification statistics**
- ▶ **Legend**

Protein Family Summary

Significance threshold p<	Max. number of families	🔗[help]
Ions score or expect cut-off	Dendrograms cut at	
Preferred taxonomy	All entries	

▶ **Sensitivity**

Proteins (30)	Report Builder	Unassigned (4449)	🔗 permalink
-------------------------------	--------------------------------	-----------------------------------	-----------------------------

Protein hits (30 proteins)

▶ **Columns:** **Standard (11 out of 16)**

▶ **Filters:** (none)

↑ <i>Family</i>	M	DB	Accession	Score	emPAI	Mass	Cov	Match(sig)	Seq(uniq+sig)	Description
1	1	SwissProt	🔗2::ALBU_BOVIN	658	0.34	71244	0.18	24	7	Albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4
2	1	SwissProt	🔗2::TRYP_PIG	170	0.60	25078	0.25	8	4	Trypsin OS=Sus scrofa OX=9823 PE=1 SV=1
3	1	SwissProt	🔗2::LYSC_PSEAB	92	0.06	48547	0.04	2	1	Lysyl endopeptidase OS=Pseudomonas aeruginosa (strain UCBPP-PA14) OX=208963 GN=prpL PE=1 SV=1
4	1	SwissProt	🔗2::IF3_BACFN	84	0.14	23349	0.04	4	1	Translation initiation factor IF-3 OS=Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / CCUG 4856 / JCM 11019 / NCTC 9343 / Onslow) OX=272559 GN=infC PE=3 SV=1
5	1	SwissProt	🔗2::THIC_NITEC	43	0.04	71463	0.01	5	1	Phosphomethylpyrimidine synthase OS=Nitrosomonas eutropha (strain DSM 101675 / C91 / Nm57) OX=335283 GN=thiC PE=3 SV=1
6	1	UB_target	🔗3::WP_013323776.1	39	0.04	87068	0.01	2	1	chromosome segregation ATPase [Gloeotheca verrucosa]
7	1	SwissProt	🔗2::MRH4_AJECN	38	0.04	70119	0.01	1	1	ATP-dependent RNA helicase MRH4, mitochondrial OS=Ajellomyces capsulatus (strain Nam1 / WU24) OX=2059318 GN=MRH4 PE=3 SV=1
8	1	SwissProt	🔗2::GUN13_ORYSI	37	0.04	68794	0.01	1	1	Endoglucanase 13 OS=Oryza sativa subsp. indica OX=39946 GN=GLU6 PE=3 SV=2
9	1	SwissProt	🔗2::PAFA_CORGB	36	0.06	53995	0.02	2	1	Pup--protein ligase OS=Corynebacterium glutamicum (strain R) OX=340322 GN=pafA PE=3 SV=1
10	1	SwissProt	🔗2::WEE2_HUMAN	35	0.05	63285	0.01	3	1	Wee1-like protein kinase 2 OS=Homo sapiens OX=9606 GN=WEE2 PE=1 SV=2
11	1	SwissProt	🔗2::GATE_METMP	33	0.04	71581	0.01	1	1	Glutamyl-tRNA(Gln) amidotransferase subunit E OS=Methanococcus maripaludis (strain S2 / LL) OX=267377 GN=gatE PE=3 SV=1
12	1	UB_target	🔗3::WP_017286765.1	33	0.11	28094	0.04	1	1	MULTISPECIES: hypothetical protein [Leptolyngbya]
13	1	SwissProt	🔗2::SYH_FINM2	32	0.06	50133	0.02	1	1	Histidine--tRNA ligase OS=Finegoldia magna (strain ATCC 29328 / DSM 20472 / WAL 2508) OX=334413 GN=hisS PE=3 SV=1
14	1	SwissProt	🔗2::ENGI_ARTBC	32	0.03	99019	0.01	2	1	Glucan endo-1,3-beta-D-glucosidase ARB_01444 OS=Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) OX=663331 GN=ARB_01444 PE=1 SV=1
15	1	SwissProt	🔗2::ZN407_HUMAN	31	0.01	251658	0.00	1	1	Zinc finger protein 407 OS=Homo sapiens OX=9606 GN=ZNF407 PE=1 SV=2
16	1	SwissProt	🔗2::SRFAA_BACSU	31	0.01	402750	0.00	1	1	Surfactin synthase subunit 1 OS= Bacillus subtilis (strain 168) OX=224308 GN=srfAA PE=1 SV=4
17	1	UB_target	🔗3::XP_059604390.1	28	0.04	79583	0.02	2	1	uncharacterized protein An12g03370 [Aspergillus niger]
18	1	SwissProt	🔗2::YL046_YEAST	28	0.10	31205	0.04	1	1	Uncharacterized membrane protein YLR046C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YLR046C PE=1 SV=1
19	1	SwissProt	🔗2::GLYR1_MOUSE	28	0.05	60248	0.02	2	1	Cytokine-like nuclear factor N-PAC OS=Mus musculus OX=10090 GN=Glyr1 PE=1 SV=1
20	1	SwissProt	🔗2::IRS4_BOTFB	27	0.03	94317	0.01	1	1	Increased rDNA silencing protein 4 OS=Botryotinia fuckeliana (strain B05.10) OX=332648 GN=irs4 PE=3 SV=1
21	1	SwissProt	🔗2::RPPH_MARN8	27	0.15	21076	0.05	1	1	RNA pyrophosphohydrolase OS=Marinobacter nauticus (strain ATCC 700491 / DSM 11845 / VT8) OX=351348 GN=rppH PE=3 SV=1
22	1	SwissProt	🔗2::NOD2_HUMAN	26	0.03	117205	0.01	1	1	Nucleotide-binding oligomerization domain-containing protein 2 OS=Homo sapiens OX=9606 GN=NOD2 PE=1 SV=1
23	1	SwissProt	🔗2::ACCA_ZYMMO	25	0.09	34417	0.02	1	1	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Zymomonas mobilis subsp. mobilis (strain ATCC 31821 / ZM4 / CP4) OX=264203 GN=acca PE=3 SV=1
24	1	SwissProt	🔗2::RS12_BLOFL	25	0.23	13876	0.07	1	1	Small ribosomal subunit protein uS12 OS=Blochmannia floridanus OX=203907 GN=rpSL PE=3 SV=1
25	1	SwissProt	🔗2::FER_METPR	25	0.91	4004	0.34	1	1	Zinc-containing ferredoxin (Fragment) OS=Metallosphaera prunae OX=47304 GN=zfx PE=1 SV=1
26	1	SwissProt	🔗2::NPL4_VANPO	25	0.05	64093	0.02	1	1	Nuclear protein localization protein 4 OS=Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294 / BCRC 21397 / CBS 2163 / NBRC 10782 / NRRL Y-8283 / UCD 57-17) OX=436907 GN=NPL4 PE=3 SV=1
27	1	SwissProt	🔗2::SEC6_SCHPO	22	0.04	86255	0.02	1	1	Exocyst complex component sec6 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=sec6 PE=1 SV=2
28	1	SwissProt	🔗2::MNMA_RICBR	22	0.08	40785	0.01	1	1	tRNA-specific 2-thiouridylase MnmA OS=Rickettsia bellii (strain RML369-C) OX=336407 GN=mnmA PE=3 SV=1
29	1	SwissProt	🔗2::ESYN_FUSEQ	21	0.01	348392	0.00	1	1	Enniatin synthase OS=Fusarium equiseti OX=61235 GN=ESYN1 PE=1 SV=2
30	1	SwissProt	🔗2::PKFA_EMENI	21	0.01	243894	0.00	1	1	Non-reducing polyketide synthase pkfA OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=pkfA PE=1 SV=1

Not what you expected? Try [🔗the select summary](#).

 MASCOT Search Results

User : Ulf Bergmann
E-mail : ub@pfa
Search title : 24B026, Univ Kiel, Hering-Peter, Sample 2 (10 ppm)
MS data file : LTQ_24B026_UnivKiel_Sample2.mgf
Databases : **1:** contaminants 20160129 (250 sequences; 129,192 residues)
2: SwissProt 2024_02 (571,282 sequences; 206,678,396 residues)
3: UB_target (60,791 sequences; 29,305,254 residues)
Timestamp : 30 Apr 2024 at 11:33:51 GMT

All Non-significant Unassigned [\[help\]](#) As XML

Not what you expected? Try [the select summary](#).

- **Search parameters**
- **Score distribution**
- **Legend**

Protein Family Summary

Significance threshold p<	Max. number of families	[help]
Ions score or expect cut-off	Dendrograms cut at	
Preferred taxonomy	All entries	

► **Sensitivity**

Proteins (15)	Report Builder	Unassigned (1762)	[permalink]
-------------------------------	----------------	-----------------------------------	-----------------------------

Protein hits (15 proteins)

► **Columns: Standard (11 out of 16)**

► **Filters: (none)**

↑ Family	M	DB	Accession	Score	emPAI	Mass	Cov	Match(sig)	Seq(uniq+sig)	Description
1	1	SwissProt	[2::TRYP_PIG	243	0.62	25078	0.25	13	4	Trypsin OS=Sus scrofa OX=9823 PE=1 SV=1
2	1	UB_target	[3::WP_013322826.1	139	0.08	38181	0.04	2	1	Fe(3+) ABC transporter substrate-binding protein [Gloeotheca verrucosa]
3	1	SwissProt	[2::LYSC_PSEAB	121	0.13	48547	0.04	3	2	Lysyl endopeptidase OS=Pseudomonas aeruginosa (strain UCBPP-PA14) OX=208963 GN=prpL PE=1 SV=1
4	1	SwissProt	[2::FMT_CHLL2	49	0.09	35122	0.03	3	1	Methionyl-tRNA formyltransferase OS=Chlorobium limicola (strain DSM 245 / NBRC 103803 / 6330) OX=290315 GN=fmt PE=3 SV=1
5	1	SwissProt	[2::SYS_ALCBS	47	0.07	48199	0.02	1	1	Serine--tRNA ligase OS=Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2) OX=393595 GN=serS PE=3 SV=1
6	1	UB_target	[3::WP_026384088.1	36	0.12	27042	0.02	1	1	hypothetical protein [Achromobacter xylosoxidans]
7	1	SwissProt	[2::DNAA_BUCCC	36	0.06	52178	0.02	1	1	Chromosomal replication initiator protein DnaA OS=Buchnera aphidicola subsp. Cinara cedri (strain Cc) OX=372461 GN=dnaA PE=3 SV=1
8	1	UB_target	[3::XP_042923141.1	36	0.02	133441	0.01	1	1	uncharacterized protein CHLRE_07g351825v5 [Chlamydomonas reinhardtii]
9	1	SwissProt	[2::CFA70_CHLRE	35	0.03	114852	0.01	1	1	Cilia- and flagella-associated protein 70 OS=Chlamydomonas reinhardtii OX=3055 GN=CFAP70 PE=1 SV=1
10	1	UB_target	[3::XP_042923599.1	34	0.04	70768	0.01	1	1	uncharacterized protein CHLRE_06g268550v5 [Chlamydomonas reinhardtii]
11	1	UB_target	[3::XP_042921092.1	32	0.02	125416	0.01	1	1	uncharacterized protein CHLRE_09g388430v5 [Chlamydomonas reinhardtii]
12	1	UB_target	[3::XP_059603708.1	28	0.10	33054	0.03	1	1	hypothetical protein An05g00150 [Aspergillus niger]
13	1	SwissProt	[2::GLYA_METJA	28	0.07	48338	0.02	1	1	Serine hydroxymethyltransferase OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=glyA PE=1 SV=1
14	1	SwissProt	[2::FKS1_CRYNH	28	0.02	205553	0.00	1	1	1,3-beta-glucan synthase component FKS1 OS=Cryptococcus neoformans var. grubii serotype A (strain H99 / ATCC 208821 / CBS 10515 / FGSC 9487) OX=235443 GN=FKS1 PE=1 SV=3
15	1	SwissProt	[2::CATB_MEDTR	22	0.08	39297	0.03	1	1	Pro-cathepsin H OS=Medicago truncatula OX=3880 GN=CP PE=1 SV=1

Not what you expected? Try [the select summary](#).

Mascot: http://www.matrixscience.com/

 MASCOT Search Results

User : Ulf Bergmann
E-mail : ub@pfa
Search title : 24B026, Univ Kiel, Hering-Peter, Sample 3 (10 ppm)
MS data file : LTQ_24B026_UnivKiel_Sample3.mgf
Databases : **1:** contaminants 20160129 (250 sequences; 129,192 residues)
2: SwissProt 2024_02 (571,282 sequences; 206,678,396 residues)
3: UB_target (60,791 sequences; 29,305,254 residues)
Timestamp : 30 Apr 2024 at 11:34:16 GMT

All Non-significant Unassigned [\[help\]](#) As XML

Not what you expected? Try [the select summary](#).

- ▶ **Search parameters**
- ▶ **Score distribution**
- ▶ **Modification statistics**
- ▶ **Legend**

Protein Family Summary

Significance threshold p<	Max. number of families	[help]
Ions score or expect cut-off	Dendrograms cut at	
Preferred taxonomy	All entries	

▶ **Sensitivity**

Proteins (57)	Report Builder	Unassigned (3803)
-------------------------------	----------------	-----------------------------------

[\[s_permalink\]](#)

Protein hits (57 proteins)

▶ **Columns: Standard (11 out of 16)**

▶ **Filters: (none)**

[†] <i>Family</i>	M	DB	Accession	Score	emPAI	Mass	Cov	Match(sig)	Seq(uniq+sig)	Description
1	1	UB_target	ef3::WP_013322826.1	276	0.08	38181	0.04	6	1	Fe(3+) ABC transporter substrate-binding protein [Gloeotheca verrucosa]
2	1	SwissProt	ef2::TRYP_PIG	173	0.60	25078	0.25	11	4	Trypsin OS=Sus scrofa OX=9823 PE=1 SV=1
3	1	SwissProt	ef2::PHAA1_NOSSI	125	0.65	17392	0.30	6	3	Allophycocyanin subunit alpha 1 OS=Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) OX=103690 GN=apcA1 PE=1 SV=3
4	1	SwissProt	ef2::LYSC_PSEAB	104	0.20	48547	0.04	5	3	Lysyl endopeptidase OS=Pseudomonas aeruginosa (strain UCBPPP-PA14) OX=208963 GN=prpL PE=1 SV=1
5	1	SwissProt	ef2::ACTA_BOVIN	79	0.07	42381	0.03	2	1	Actin, aortic smooth muscle OS=Bos taurus OX=9913 GN=ACTA2 PE=1 SV=1
6	1	SwissProt	ef2::FKBP_CRYNB	68	0.28	11716	0.07	2	1	FK506-binding protein 1 OS=Cryptococcus neoformans var. neoformans serotype D (strain B-3501A) OX=283643 GN=FPRI PE=3 SV=1
7	1	SwissProt	ef2::IRS4_BOTFB	55	0.03	94317	0.01	3	1	Increased rDNA silencing protein 4 OS=Botryotinia fuckeliana (strain B05.10) OX=332648 GN=irs4 PE=3 SV=1
8	1	UB_target	ef3::WP_013321747.1	54	0.10	30919	0.07	2	1	phycobilisome linker polypeptide [Gloeotheca verrucosa]
9	1	UB_target	ef3::WP_017288649.1	49	0.11	28759	0.03	2	1	MULTISPECIES: phycobilisome rod-core linker polypeptide [Leptolyngbya]
10	1	SwissProt	ef2::VERU1_PENPO	48	0.08	40374	0.03	2	1	Terpene cyclase verU1 OS=Penicillium polonicum OX=60169 GN=verU1 PE=3 SV=1
11	1	UB_target	ef3::XP_042920615.1	48	0.05	61711	0.02	1	1	uncharacterized protein CHLRE_10g464264v5 [Chlamydomonas reinhardtii]
12	1	SwissProt	ef2::ADDB_CARHZ	45	0.02	124525	0.01	3	1	ATP-dependent helicase/deoxyribonuclease subunit B OS=Carboxydotherrmus hydrogenoformans (strain ATCC BAA-161 / DSM 6008 / Z-2901) OX=246194 GN=addB PE=3 SV=1
13	1	SwissProt	ef2::WFDC3_MOUSE	42	0.22	14621	0.05	1	1	WAP four-disulfide core domain protein 3 OS=Mus musculus OX=10090 GN=Wfdc3 PE=2 SV=1
14	1	SwissProt	ef2::PYR1_SYNY3	41	0.10	32501	0.02	1	1	Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated, rod 1 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=cpcC1 PE=1 SV=3
15	1	SwissProt	ef2::WEE2_HUMAN	41	0.05	63285	0.01	2	1	Wee1-like protein kinase 2 OS=Homo sapiens OX=9606 GN=WEE2 PE=1 SV=2
16	1	SwissProt	ef2::RRF_RHIWR	40	0.16	20298	0.05	2	1	Ribosome-recycling factor OS=Rhizorhabdus wittichii (strain DSM 6014 / CCUG 31198 / JCM 15750 / NBRC 105917 / EY 4224 / RW1) OX=392499 GN=frf PE=3 SV=1
17	1	SwissProt	ef2::RECF_CHLFF	40	0.07	42190	0.02	2	1	DNA replication and repair protein RecF OS=Chlamydia felis (strain Fe/C-56) OX=264202 GN=recF PE=3 SV=1
18	1	SwissProt	ef2::ZAR1_ARATH	40	0.04	79284	0.01	1	1	Receptor protein kinase-like protein ZAR1 OS=Arabidopsis thaliana OX=3702 GN=ZAR1 PE=1 SV=1
19	1	UB_target	ef3::WP_013323776.1	39	0.04	87068	0.01	2	1	chromosome segregation ATPase [Gloeotheca verrucosa]
20	1	SwissProt	ef2::PGK_SULAC	39	0.07	45429	0.02	1	1	Phosphoglycerate kinase OS=Sulfolobus acidocaldarius (strain ATCC 33909 / DSM 639 / JCM 8929 / NBRC 15157 / NCIMB 11770) OX=330779 GN=pgk PE=3 SV=1
21	1	SwissProt	ef2::TFE_META3	38	0.15	20756	0.04	3	1	Transcription factor E OS=Methanococcus aeolicus (strain ATCC BAA-1280 / DSM 17508 / OCM 812 / Nankai-3) OX=419665 GN=tfe PE=3 SV=2
22	1	UB_target	ef3::XP_042927163.1	38	0.02	129410	0.01	2	1	uncharacterized protein CHLRE_02g095059v5 [Chlamydomonas reinhardtii]
23	1	SwissProt	ef2::CCMK2_THEVB	37	0.30	10900	0.18	1	1	Carboxysome shell protein CcmK2 OS=Thermosynechococcus vestitus (strain NIES-2133 / IAM M-273 / BP-1) OX=197221 GN=ccmK2 PE=1 SV=1
24	1	SwissProt	ef2::CXAR_BOVIN	37	0.08	40641	0.02	1	1	Coxsackievirus and adenovirus receptor homolog OS=Bos taurus OX=9913 GN=CXADR PE=2 SV=1
25	1	SwissProt	ef2::DYHC_DICDI	36	0.01	541613	0.00	1	1	Dynein heavy chain, cytoplasmic OS=Dictyostelium discoideum OX=44689 GN=dhcA PE=1 SV=2
26	1	SwissProt	ef2::RL27_ALIF1	36	0.36	9175	0.09	1	1	Large ribosomal subunit protein bL27 OS=Aliivibrio fischeri (strain ATCC 700601 / ES114) OX=312309 GN=rpma PE=3 SV=1
27	1	SwissProt	ef2::RISB_CLOBA	36	0.19	16478	0.07	1	1	6,7-dimethyl-8-ribityllumazine synthase OS=Clostridium botulinum (strain Alaska E43 / Type E3) OX=508767 GN=ribH PE=3 SV=1
28	1	UB_target	ef3::XP_059601156.1	35	0.03	122504	0.01	1	1	uncharacterized protein An08g01810, partial [Aspergillus niger]
29	1	SwissProt	ef2::SLA1_VANPO	35	0.02	131386	0.01	1	1	Actin cytoskeleton-regulatory complex protein SLA1 OS=Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294 / BCRC 21397 / CBS 2163 / NBRC 10782 / NRRL Y-8283 / UCD 57-17) OX=436907 GN=SLA1 PE=3 SV=1
30	1	UB_target	ef3::WP_247219987.1	35	0.07	43509	0.02	1	1	amino acid ABC transporter permease [Shinella oryzae]
31	1	SwissProt	ef2::HSB1_PICST	34	0.23	14252	0.07	1	1	Histone H2B.1 OS=Scheffersomyces stipitis (strain ATCC 58785 / CBS 6054 / NBRC 10063 / NRRL Y-11545) OX=322104 GN=HTB1 PE=3 SV=1
32	1	SwissProt	ef2::SSRP_HRRRG	34	0.18	17452	0.05	1	1	SsrA-binding protein OS=Ehrlichia ruminantium (strain Gardel) OX=302409 GN=ssmpB PE=3 SV=1
33	1	SwissProt	ef2::SYA_BUCAP	34	0.03	102794	0.01	1	1	Alanine--tRNA ligase OS=Buchnera aphidicola subsp. Schizaphis graminum (strain Sg) OX=198804 GN=alaS PE=3 SV=1
34	1	SwissProt	ef2::ENG1_ARTBC	33	0.03	90719	0.01	2	1	Glucan endo-1,3-beta-D-glucosidase ARB_01444 OS=Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) OX=663331 GN=ARB_01444 PE=1 SV=1
35	1	SwissProt	ef2::YPEB_BACSU	31	0.06	51210	0.02	1	1	Sporulation protein YpeB OS=Bacillus subtilis (strain 168) OX=224308 GN=ypeB PE=1 SV=2
36	1	SwissProt	ef2::PTH_GEOSL	31	0.15	20930	0.03	1	1	Peptidyl-tRNA hydrolase OS=Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) OX=243231 GN=pth PE=3 SV=1
37	1	SwissProt	ef2::DAPAL_PYRIL	30	0.09	33262	0.02	1	1	Uncharacterized DapA-like lyase PlsI_0309 OS=Pyrobaculum islandicum (strain DSM 4184 / JCM 9189 / GEO3) OX=384616 GN=dapAL PE=3 SV=2
38	1	SwissProt	ef2::GLH4_CAEEL	30	0.03	121764	0.01	1	1	ATP-dependent RNA helicase glh-4 OS=Caenorhabditis elegans OX=6239 GN=glh-4 PE=1 SV=2
39	1	UB_target	ef3::WP_054514275.1	30	0.06	52562	0.03	2	1	aldehyde dehydrogenase family protein [Achromobacter xylosoxidans]
40	1	SwissProt	ef2::GLMS_LEPIC	29	0.05	68299	0.01	1	1	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni (strain Fiocruz L1-130) OX=267671 GN=glms PE=3 SV=3
41	1	SwissProt	ef2::PLUA_STREE	29	0.02	143229	0.01	1	1	Pullulanase A OS=Streptococcus pneumoniae OX=1313 GN=spuA PE=1 SV=1
42	1	SwissProt	ef2::SMC6_YEAST	29	0.02	128557	0.01	1	1	Structural maintenance of chromosomes protein 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288C) OX=559292 GN=SMC6 PE=1 SV=1
43	1	SwissProt	ef2::GFOD1_HUMAN	27	0.07	43700	0.03	2	1	Glucose-fructose oxidoreductase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=GFOD1 PE=1 SV=1

44	1	SwissProt	ef2::RSMH_RHOPB	27	0.09	34882	0.05	1	1	Ribosomal RNA small subunit methyltransferase H OS=Rhodospseudomonas palustris (strain BisB18) OX=316056 GN=rsmH PE=3 SV=1
45	1	SwissProt	ef2::NPL4_VANPO	27	0.05	64093	0.02	2	1	Nuclear protein localization protein 4 OS=Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294 / BCRC 21397 / CBS 2163 / NBRC 10782 / NRRL Y-8283 / UCD 57-17) OX=436907 GN=NPL4 PE=3 SV=1
46	1	SwissProt	ef2::SYE_METVS	26	0.05	64532	0.02	2	1	Glutamate--tRNA ligase OS=Methanococcus vannielii (strain ATCC 35089 / DSM 1224 / JCM 13029 / OCM 148 / SB) OX=406327 GN=gltX PE=3 SV=1
47	1	SwissProt	ef2::SULP3_CAEEL	26	0.03	88160	0.02	1	1	Sulfate permease family protein 3 OS=Caenorhabditis elegans OX=6239 GN=sulp-3 PE=2 SV=3
48	1	SwissProt	ef2::RN227_MOUSE	25	0.15	21320	0.05	1	1	RING finger protein 227 OS=Mus musculus OX=10090 GN=Rnf227 PE=2 SV=2
49	1	SwissProt	ef2::L_TAMVU	25	0.01	258073	0.01	1	1	RNA-directed RNA polymerase L OS=Tamiami mammarenavirus (isolate Rat/United States/W 10777/1964) OX=3052329 GN=L PE=3 SV=1
50	1	SwissProt	ef2::DHSL_COXBN	25	0.08	39944	0.02	1	1	Deoxyhypusine synthase-like protein OS=Coxiella burnetii (strain Dugway 5J108-111) OX=434922 GN=CBUD_0732 PE=3 SV=1
51	1	SwissProt	ef2::PORTL_BPSP1	25	0.05	57696	0.03	1	1	Probable portal protein OS=Bacillus phage SP01 OX=2884427 GN=3.1 PE=3 SV=1
52	1	SwissProt	ef2::SETX_HUMAN	24	0.01	307022	0.00	1	1	Probable helicase senataxin OS=Homo sapiens OX=9606 GN=SETX PE=1 SV=4
53	1	SwissProt	ef2::KDSB_PSYCK	23	0.10	29894	0.03	1	1	3-deoxy-manno-octulosonate cytidyllyltransferase OS=Psychrobacter cryohalolentis (strain ATCC BAA-1226 / DSM 17306 / VKM B-2378 / K5) OX=335284 GN=kdsB PE=3 SV=1
54	1	SwissProt	ef2::POTA_MYCS5	22	0.06	53941	0.02	1	1	Spermidine/putrescine import ATP-binding protein PotA OS=Mycoplasmopsis synoviae (strain 53) OX=262723 GN=potA PE=3 SV=2
55	1	UB_target	ef3::WP_017286940.1	22	0.10	32387	0.02	1	1	MULTISPECIES: formyltetrahydrofolate deformylase [Leptolyngbya]
56	1	SwissProt	ef2::NRDG_SALTI	22	0.18	17735	0.05	1	1	Anaerobic ribonucleoside-triphosphate reductase-activating protein OS=Salmonella typhi OX=90370 GN=nrdG PE=3 SV=1
57	1	SwissProt	ef2::DBP7_EMENI	21	0.04	85504	0.02	1	1	ATP-dependent RNA helicase dbp7 OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=dbp7 PE=3 SV=1

Not what you expected? Try [the select summary](#).

Mascot: <http://www.matrixscience.com/>